

UNIVERSITI TEKNOLOGI MARA

**CHARACTERIZATION OF
N-ACETYLGLUCOSAMINIDASE GENE
FROM
*Staphylococcus aureus***

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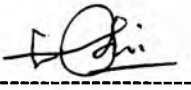
MSc

September 2014

AUTHOR'S DECLARATION

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ABSTRACT

SACOL2666, which is known as an N-acetylmuramoyl-L-alanine in NCBI database is shown to be homologous with *atl* of *S. aureus*, a bifunctional autolysin gene. In this study, *in-silico* analysis of deduced amino acids sequence *SACOL2666* was characterized to confirm the protein from *S. aureus* SH1000 is an *N*-acetylglucosaminidase autolysin. Successful transformed gene in pBAD-sScaB and pQE60-xScaQ clones contain 1860 bp of the full gene and 1779 bp of gene without signal peptide sequence. An *N*-acetylglucosaminidase protein family (PF01832) of Lysozyme-like superfamily is found in *SACOL2666* domain architecture. The amino acid of *SACOL2666* gene demonstrated a high sequence similarity to characterized *N*-acetylglucosaminidases, AcmB (*L. lactis*) and Auto (*L. monocytogenes*) Group B in GH73 rather than bifunctional autolysins in Group A, Atl (*S. aureus*). *SACOL2666* has high relatedness in sequence similarity (46%) and structural alignment with *N*-acetylglucosaminidases Auto Chain A structure (3FI7_A). Residue E352, G356, E386, F399, Y455 and a tetrad YATD (Y449-D452) at *SACOL2666* hypothetical secondary structures are shown to be identical to Auto (3FI7_A) residues. As conclusion, this study reveals *SACOL2666* as a novel *N*-acetylglucosaminidase with high sequence similarity to *N*-acetylglucosaminidases in Group B of GH73. Moreover, structural similarity suggests the functional and enzymatic activity of *SACOL2666* is similar to Auto (3FI7_A).

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